

RAW SEQUENCE LISTING

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Application Serial Number: 101812, 849A
Source: IFW/K
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IFW16

RAW SEQUENCE LISTING

DATE: 04/27/2007

PATENT APPLICATION: US/10/812,849A

TIME: 11:34:00

Input Set : A:\40037.txt

Output Set: N:\CRF4\04272007\J812849A.raw

3 <110> APPLICANT: Zankel et al.

5 <120> TITLE OF INVENTION: MEGALIN-BASED DELIVERY OF THERAPEUTIC COMPOUNDS
TO THE BRAIN AND

6 OTHER TISSUES

8 <130> FILE REFERENCE: 31075/40037

10 <140> CURRENT APPLICATION NUMBER: 10/812,849A

11 <141> CURRENT FILING DATE: 2004-03-30

13 <150> PRIOR APPLICATION NUMBER: US 10/600,862

14 <151> PRIOR FILING DATE: 2003-06-20

16 <160> NUMBER OF SEQ ID NOS: 29

18 <170> SOFTWARE: PatentIn version 3.2

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 323

22 <212> TYPE: PRT

23 <213> ORGANISM: Homo sapiens

25 <400> SEQUENCE: 1

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28 1 5 10 15

31 Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala

32 20 25 30

35 Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp

36 35 40 45

39 Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu

40 50 55 60

43 Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn

44 65 70 75 80

47 Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala

48 85 90 95

51 Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu

52 100 105 110

55 Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly

56 115 120 125

59 Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His

60 130 135 140

64 His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser

65 145 150 155 160

68 Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser

69 165 170 175

72 Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu

73 180 185 190

76 Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser

77 195 200 205

80 His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile

81 210 215 220

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84 Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu
85 225                230                235                240
88 Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys
89                245                250                255
92 His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg
93                260                265                270
96 His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu
97                275                280                285
100 Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val
101                290                295                300
104 Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His
105 305                310                315                320
107 Asn Glu Leu
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112 <211> LENGTH: 209
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
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119 1                5                10                15
122 Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His His Lys
123                20                25                30
126 Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser Arg Thr
127                35                40                45
130 Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser Asp Ile
131                50                55                60
134 Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu Lys Leu
135 65                70                75                80
138 Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser His Gln
139                85                90                95
142 Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile Asp Leu
143                100               105               110
146 Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu Glu Ala
147                115               120               125
150 Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn
151                130               135               140
154 His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg His Ala
155 145                150                155                160
158 Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu Lys His
159                165                170                175
162 Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val Lys Lys
163                180                185                190
166 His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His Asn Glu
167                195                200                205
170 Leu
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175 <211> LENGTH: 33
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial sequence

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180 <223> OTHER INFORMATION: Synthetic primer
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187 <211> LENGTH: 35
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Synthetic primer
194 <400> SEQUENCE: 4
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199 <211> LENGTH: 205
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo sapiens
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206 1 5 10 15
209 Val Arg Leu Thr Ser Cys Ala Arg Val Leu His Tyr Lys Glu Lys Ile
210 20 25 30
213 His Glu Tyr Asn Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly
214 35 40 45
217 Tyr Glu Asn Leu Leu Ser Pro Ser Asp Met Thr His Ile Lys Ser Asp
218 50 55 60
221 Thr Leu Ala Ser Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile
222 65 70 75 80
225 Asn Gln Gly Leu Asp Arg Leu Arg Lys Val Ser His Gln Leu Arg Pro
226 85 90 95
229 Ala Thr Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala
230 100 105 110
233 Gln Ser Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu
234 115 120 125
237 Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys
238 130 135 140
241 Gln Leu Glu Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly
242 145 150 155 160
245 Asp Pro Glu His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu
246 165 170 175
249 Glu Lys Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp
250 180 185 190
253 Leu Ser Ser Arg Val Ser Arg Ala Arg His Asn Glu Leu
254 195 200 205
257 <210> SEQ ID NO: 6
258 <211> LENGTH: 3702
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: RAP-GAA fusion sequence

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268 ctcgatcct actcgcgga gaagaaccag cccaagccgt ccccgaaacg cgagtcggga      120
270 gaggagtcc gcatggagaa gttgaaccag ctgtgggaga agggccagcg actgcatctt      180
272 cctcccgtga ggctggccga gctccacgct gatctgaaga tacaggagag ggacgaactc      240
274 gcctggaaga aactaaagct tgacggcttg gacgaagatg gggagaagga agcgagactc      300
276 atacgcaacc tcaatgtcat cttggccaag tatggtctgg acggaaagaa ggacgctcgg      360
278 caggtgacca gcaactccct cagtggcacc caggaagacg ggctggatga ccccgagctg      420
280 gaaaagctgt ggcacaaggc gaagacctct gggaaattct ccggcgaaga actggacaag      480
282 ctctggcggg agttcctgca tcacaaagag aaagttcacg agtacaacgt cctgctggag      540
284 accctgagca ggaccgaaga aatccacgag aacgtcatta gcccctcgga cctgagcgac      600
286 atcaagggca gcgtcctgca cagcaggcac acggagctga aggagaagct gcgcagcatc      660
288 aaccagggcc tggaccgcct gcgcagggtc agccaccagg gctacagcac tgaggctgag      720
290 ttcgaggagc ccagggtgat tgacctgtgg gacctggcgc agtccgcaa cctcacggac      780
292 aaggagctgg aggcgttccg ggaggagctc aagcacttcg aagccaaaat cgagaagcac      840
294 aaccactacc agaagcagct ggagattgcg caggagaagc tgaggcacgc agagagcgtg      900
296 ggcgacggcg agcgtgtgag ccgcagccgc gagaagcacg ccctgctgga ggggaggacc      960
298 aaggagctgg gctacacggt gaagaagcat ctgcaggacc tgtccggcag gatctccaga     1020
300 gctcgcgccg aggcagaaac cggtgcacac cccggccgtc ccagagcagt gcccacacag     1080
302 tgcgacgtcc cccccaacag ccgcttcgat tgcgccccctg acaaggccat caccagggaa     1140
304 cagtcgagag cccgcggctg ctgctacatc cctgcaaagc aggggctgca gggagcccag     1200
306 atggggcagc cctggtgctt cttcccaccc agctacccca gctacaagct ggagaacctg     1260
308 agtcctctg aaatgggcta cacggccacc ctgaccgta ccacccccac cttcttcccc     1320
310 aaggacatcc tgacctgcg gctggacgtg atgatggaga ctgagaaccg cctccacttc     1380
312 acgatcaaag atccagctaa caggcgctac gaggtgccct tggagacccc gcgtgtccac     1440
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316 gtgcaccggc agctggacgg ccgctgtctg ctgaacacga cgggtggcgc cctgttcttt     1560
318 gcggaccagt tccttcagct gtccacctcg ctgccctcgc agtatatcac aggcctcgcc     1620
320 gagcacctca gtcccctgat gctcagcacc agctggacca ggatcaccct gtggaaccgg     1680
322 gaccttgccg ccacgcccgg tgcgaacctc tacgggtctc accctttcta cctggcgctg     1740
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326 ctgcagccga gccctgccct tagctggagg tcgacagggt ggatcctgga tgtctacatc     1860
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332 gctatcccc gccaggtggt ggagaacatg accagggccc acttccccct ggacgtccaa     2040
334 tggaacgacc tggactacat ggactcccgg agggacttca cgttcaacaa ggatggcttc     2100
336 cgggacttcc cggccatggt gcaggagctg caccagggcg gccggcgcta catgatgatc     2160
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342 cccgggtcca ctgccttccc cgacttcacc aaccccacag ccctggcctg gtgggaggac     2340
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346 ccttccaact tcatcagagg ctctgaggac ggctgcccc acaatgagct ggagaaccca     2460
348 ccctacgtgc ctgggggtgt tggggggacc ctccaggcgg ccaccatctg tgccctccagc     2520
350 caccagtttc tctccacaca ctacaacctg cacaacctct acggcctgac cgaagccatc     2580
352 gcctcccaca gggcgctggt gaaggctcgg gggacacgcc catttgatgat ctccgctcg     2640
354 acctttgctg gccacggccg atacgccggc cactggacgg gggacgtgtg gagctcctgg     2700
356 gagcagctcg cctcctccgt gccagaaatc ctgcagttta acctgctggg ggtgcctctg     2760
358 gtcggggccg acgtctgcgg cttcctgggc aacacctcag aggagctgtg tgtgcgctgg     2820
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362 caggagccgt acagcttcag cgagccggcc cagcaggcca tgaggaaggc cctcaccctg 2940
364 cgctacgcac tcctccccc cctctacaca ctgttcacc aggccacgt cgcgggggag 3000
366 accgtggccc ggcccctctt cctggagttc cccaaggact ctagcacctg gactgtggac 3060
368 caccagctcc tgtgggggga ggccctgctc atcaccacag tgctccaggc cggaaggcc 3120
370 gaagtgactg gctacttccc cttgggcaca tggtagacc tgcagacggt gccaatagag 3180
372 gcccttggca gcctcccacc cccacctgca gctcccctg agccagccat ccacagcgag 3240
374 gggcagtggg tgacgtgcc ggccccctg gacaccatca acgtccacct ccgggctggg 3300
376 tacatcatcc ccctgcaggg ccctggcctc acaaccacag agtcccgcga gcagcccatg 3360
378 gccctggctg tggccctaac caagggtgga gaggcccag gggagctgtt ctgggacgat 3420
380 ggagagagcc tggaagtgt ggagcgagg gcctacacac aggtcatctt cctggccagg 3480
382 aataacacga tcgtgaatga gctggtacgt gtgaccagt agggagctgg cctgcagctg 3540
384 cagaagggtga ctgtcctggg cgtggccacg gcgccccagc aggtcctctc caacggtgtc 3600
386 cctgtctcca acttcaccta cagccccgac accaaggtcc tggacatctg tgtctcgtg 3660
388 ttgatgggag agcagtttct cgtcagctgg tgttgactcg ag 3702
391 <210> SEQ ID NO: 7
392 <211> LENGTH: 1228
393 <212> TYPE: PRT
394 <213> ORGANISM: Artificial sequence
396 <220> FEATURE:
397 <223> OTHER INFORMATION: RAP-GAA fusion sequence
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405 Val Leu Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro
406 20 25 30
409 Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu
410 35 40 45
413 Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu
414 50 55 60
417 Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys
418 65 70 75 80
421 Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg
422 85 90 95
425 Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly
426 100 105 110
429 Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln
430 115 120 125
433 Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala
434 130 135 140
437 Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg
438 145 150 155 160
441 Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu
442 165 170 175
445 Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro
446 180 185 190
449 Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr
450 195 200 205
453 Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu
454 210 215 220

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